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Randal J. Kaufman
07/621,092
November 30, 1990

JAN 18 1991

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

#2

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). However, this application fails to comply with one or more of the requirements of 37 CFR §§ 1.821 through 1.825 as follows:

- ☐ 1. This application clearly fails to comply with the collective requirements of §§ 1.821 through 1.825. Applicant's attention is directed to these regulations, a copy of which is attached.
- ☐ 2. This application does not conform exclusively to the requirements of §§ 1.821 through 1.825. The non-conforming material should be deleted. § 1.821(b).
- ☐ 3. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." § 1.821(c).
- ☐ 4. This application does contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." However, the "Sequence Listing" does not comply with the requirements of §§ 1.821 through 1.825 as follows:
 - ☐ a. The sequence data does not comply with the symbol and format requirements of paragraphs (b) through (p) of § 1.822. Specifically: _____
 - ☐ b. The "Sequence Listing" does not comply with the location and page requirements of paragraph (a) of § 1.823.
 - ☐ c. The "Sequence Listing" does not comply with the information requirements of paragraph (b) of § 1.823. Specifically: _____
 - ☐ d. Other: _____
- ☐ 5. The description and/or claims of the patent application mention a sequence that is set forth in the "Sequence Listing" but reference is not properly made to the sequence by use of a sequence identifier as required by § 1.821(d).
- ☐ 6. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by § 1.821(e).
- ☒ 7. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the computer readable form does not comply with the requirements of § 1.824. Specifically: SEE ATTACHED "RAW SEQUENCE LISTING".
- ☐ 8. A statement that the content of the paper and computer readable copies are the same has not been submitted as required by § 1.821(f).
- ☐ 9. The amendment to or replacement of the paper and/or computer readable copies of the "Sequence Listing" does not comply with the requirements of § 1.825(a) through (c).
- ☐ 10. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable. Applicant must provide a substitute copy of the data in computer readable form accompanied by a statement that the substitute data is identical to that originally filed. § 1.825(d). Specifically: _____
- ☐ 11. Other: _____

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE ABOVE REQUIREMENTS. Failure to comply with the above requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR § 1.136. Direct the response to, and any questions about, this notice to the undersigned. A copy of this notice MUST be returned with your response.

Dora Straud
For: Manager, Application Processing Division
(703) 303-1202 or 303-1203

☐ Examining Group
(03) 308-

#6

Raw Sequence Listing
Patent Application US/07/621,092A

01/24/91
08:57:44

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kaufman, Randal J.
Wasley, Louise

(ii) TITLE OF INVENTION: Method of Increasing Yield of
Mature Proteins

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: United States of America
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 07/621092
(B) FILING DATE: 26-NOV-1990
(C) CLASSIFICATION: 424

(vii) PRIOR APPLICATION DATA: not applicable

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION

(A) NAME: Ellen J. Kapinos, Esquire
(B) REGISTRATION NUMBER: 32,245
(C) REFERENCE/DOCKET NUMBER: GI 5181

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54 (ix) TELECOMMUNICATION INFORMATION:
55
56 (A) TELEPHONE: (617) 876-1170
57 (B) TELEFAX: (617) 876-5851
58
59 (2) INFORMATION FOR SEQ ID NO:1
60
61 (i) SEQUENCE CHARACTERISTICS:
62
63 (A) LENGTH: 2385 base pairs
64
65 (B) TYPE: nucleic acid
66
67 (C) STRANDEDNESS: double
68
69 (D) Topology: unknown
70
71 (ii) MOLECULE TYPE: partial human genomic DNA
72
73 (A) DESCRIPTION: sequence encoding furin
74
75 (iii) HYPOTHETICAL: no
76
77 (iv) ANTI-SENSE: no
78
79 (v) PUBLICATION INFORMATION: A.M.W. van den Ouweland et
80 al, Nucl. Acids. Res., 18:664 (1990)
81
82 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:1
83
84 ATG GAG CTC AGG CCC TGG TTC 21
85 Met Glu Leu Arg Pro Trp Leu
86 1 5
87
88 CTA TGG GTC GTA CCA CCA ACA GGA ACC TTG GTC CTG CTA 60
89 Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu
90 10 15 20
91
92 GCA GCT GAT GCT CAG GGC CAG AAG GTC TTC ACC AAC ACG 99
93 Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr
94 25 30
95
96 TGG GCT GTG CGC ATC CCT GGA GGC CCA GCG GTG GCC AAC 138
97 Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn
98 35 40 45
99
100
101 AGT GTG GCA CGG AAG CAT GGG TTC CTC AAC CTG GGC CAG 177
102 Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln
103 50 55
104
105 ATC TTC GGG GAC TAT TAC CAC TTC TGG CAT CGA GGA GTG 216
106 Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val

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	60	65	70	
107				
108				
109				
110	ACG AAG CGG TCC CTG TCG CCT CAC CGC CCG CGG CAC AGC			255
111	Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser			
112	75	80	85	
113				
114				
115	CGG CTG CAG AGG GAG CCT CAA GTA CAG TGG CTG GAA CAG			294
116	Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln			
117	90	95		
118				
119	CAG GTG GCA AAG CGA CGG ACT AAA CGG GAC GTG TAC CAG			333
120	Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln			
121	100	105	110	
122				
123	GAG CCC ACA GAC CCC AAG TTT CCT CAG CAG TGG TAC CTG			372
124	Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu			
125	115	120		
126				
127	TCT GGT GTC ACT CAG CGG GAC CTG AAT GTG AAG GCG GCC			411
128	Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala			
129	125	130	135	
130				
131	TGG GCG CAG GGC TAC ACA GGG CAC GGC ATT CTG GTC TCC			450
132	Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser			
133	140	145	150	
134				
135	ATT CTG GAC GAT GGC ATC GAG AAG AAC CAC CCC GAC TTG			489
136	Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu			
137	155	160		
138				
139	GCA GGC AAT TAT GAT CCT GGG GCC AGT TTT CAT GTC AAT			528
140	Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn			
141	165	170	175	
142				
143	GAC CAG GAC CCT GAC CCC CAG CCT CGG TAC ACA CAG ATG			567
144	Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met			
145	180	185		
146				
147	AAT GAC AAC AGG CAC GGC ACA CGG TGT GCG GGG GAA GTG			606
148	Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val			
149	190	195	200	
150				
151	GCT GCC GTG GCC AAC AAC CGT GTC TGT GGT GTA GGT GTG			645
152	Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val			
153	205	210	215	
154				
155	GCC TAC AAC GCC CGC ATT GGA GGG GTC CGC ATG CTG GAT			684
156	Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp			
157	220	225		
158				
159	GGC GAG GTG ACA GAT GCA GTG GAG GCA CGC TCG CTG GGC			723

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160	Gly	Glu	Val	Thr	Asp	Ala	Val	Glu	Ala	Arg	Ser	Leu	Gly	
161		230					235					240		
162														
163	CTG	AAC	CCC	AAC	CAC	ATC	CAC	ATC	TAC	AGT	GCC	AGC	TGG	762
164	Leu	Asn	Pro	Asn	His	Ile	His	Ile	Tyr	Ser	Ala	Ser	Trp	
165				245					250					
166														
167	GGC	CCC	GAG	GAT	GAC	GGC	AAG	ACA	GTG	GAT	GGG	CCA	GCC	801
168	Gly	Pro	Glu	Asp	Asp	Gly	Lys	Thr	Val	Asp	Gly	Pro	Ala	
169	255					260					265			
170														
171	CGG	CTC	GCC	GAG	GAG	GCC	TTC	TTC	CGT	GGG	CTT	AGC	CAG	840
172	Arg	Leu	Ala	Glu	Glu	Ala	Phe	Phe	Arg	Gly	Val	Ser	Gln	
173			270					275					280	
174														
175	GGC	CGA	GGG	GGG	CTG	GGC	TCC	ATC	TTT	GTC	TGG	GCC	TCG	879
176	Gly	Arg	Gly	Gly	Leu	Gly	Ser	Ile	Phe	Val	Trp	Ala	Ser	
177					285					290				
178														
179	GGG	AAC	GGG	GGG	CGG	GAA	CAT	GAC	AGC	TGC	AAC	TGC	GAC	918
180	Gly	Asn	Gly	Gly	Arg	Glu	His	Asp	Ser	Cys	Asn	Cys	Asp	
181		295					300					305		
182														
183	GGC	TAC	ACC	AAC	AGT	ATC	TAC	ACG	CTG	TCC	ATC	AGC	AGC	957
184	Gly	Tyr	Thr	Asn	Ser	Ile	Tyr	Thr	Leu	Ser	Ile	Ser	Ser	
185				310					315					
186														
187	GCC	ACG	CAG	TTT	GGC	AAC	GTG	CCG	TGG	TAC	AGC	GAG	GCC	996
188	Ala	Thr	Gln	Phe	Gly	Asn	Val	Pro	Trp	Tyr	Ser	Glu	Ala	
189	320					325					330			
190														
191	TGC	TCG	TCC	ACA	CTG	GCC	ACG	ACC	TAC	AGC	AGT	GGC	AAC	1035
192	Cys	Ser	Ser	Thr	Leu	Ala	Thr	Thr	Tyr	Ser	Ser	Gly	Asn	
193			335					340					345	
194														
195	CAG	AAT	GAG	AAG	CAG	ATC	GTG	ACG	ACT	GAC	TTG	CGG	CAG	1074
196	Gln	Asn	Glu	Lys	Gln	Ile	Val	Thr	Thr	Asp	Leu	Arg	Gln	
197					350					355				
198														
199	AAG	TGC	ACG	GAG	TCT	CAC	ACG	GGC	ACC	TCA	GCC	TCT	GCC	1113
200	Lys	Cys	Thr	Glu	Ser	His	Thr	Gly	Thr	Ser	Ala	Ser	Ala	
201		360					365				370			
202														
203	CCC	TTA	GCA	GCC	GGC	ATC	ATT	GCT	CTC	ACC	CTG	GAG	GCC	1152
204	Pro	Leu	Ala	Ala	Gly	Ile	Ile	Ala	Leu	Thr	Leu	Glu	Ala	
205				375					380					
206														
207	AAT	AAG	AAC	CTC	ACA	TGG	CGG	GAC	ATG	CAA	CAC	CTG	GTG	1191
208	Asn	Lys	Asn	Leu	Thr	Trp	Arg	Asp	Met	Gln	His	Leu	Val	
209	385					390					395			
210														
211	GTA	CAG	ACC	TCG	AAG	CCA	GCC	CAC	CTC	AAT	GCC	AAC	GAC	1230
212	Val	Gln	Thr	Ser	Lys	Pro	Ala	His	Leu	Asn	Ala	Asn	Asp	

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	400	405	410	
213				
214				
215	TGG GCC ACC AAT GGT GTG GGG CGG AAA GTG AGC CAC TCA			1269
216	Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser			
217		415	420	
218				
219	TAT GGC TAC GGG CTT TTC GAC GCA GGC GCC ATG GTG GCC			1308
220	Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala			
221		425	430	435
222				
223	CTG GCC CAG AAT TGG ACC ACA GTC GCC CCC CAG CGG AAG			1347
224	Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys			
225		440	445	
226				
227	TGC ATC ATC GAC ATC CTC ACC GAG CCC AAA GAC ATC GGG			1386
228	Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly			
229		450	455	460
230				
231	AAA CGG CTC GAC CTC CGG AAC ACC GTG ACC GCG TCC CTG			1425
232	Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu			
233		465	470	475
234				
235	GGC GAG CCC AAC CAC ATC ACT CGG CTG GAG CAC GCT CAG			1464
236	Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln			
237		480	485	
238				
239	GCG CGG CTC ACC CTG TCC TAT AAT CGC CGT GGC GAC CTG			1503
240	Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu			
241		490	495	500
242				
243	GCC ATC CAC CTG GTC AGC CCC ATG GGC ACC CGC TCC ACC			1542
244	Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr			
245		505	510	
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247	CTG CTG GCA GCC AGG CCA CAT GAC TAC TCC GCA GAT GGG			1581
248	Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly			
249		515	520	525
250				
251	TTT AAT GAC TGG GCC TTC ATG ACA ACT CAT TCC TGG GAT			1620
252	Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp			
253		530	535	540
254				
255	GAC GAT CCC TCT GGG GAG TGG GTC CTA GAG ATT GAA AAC			1659
256	Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn			
257		545	550	
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259	ACC AGC GAA GCC AAC AAC TAT GGG ACG CTG ACC AAC TCC			1698
260	Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe			
261		555	560	565
262				
263	ACC CTC GTA CTC TAT GGC ACC GCC CCT GAC GGG CTC CCC			1737
264	Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro			
265		570	575	

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266
267   GTA CCT CCA GAA AGC AGT GGC TGC AAG ACC CTC ACG TCC   1776
268   Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
269   580                               585                               590
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271   AGT CAG GCC TGT GTG GTG TGC GAG GAA GGC TTC TCC CTC   1815
272   Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
273           595                               600                               605
274
275   CAC CAG AAG AGC TGT GTC CAG CAC TGC CCT CCA GGC TTC   1854
276   His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
277           610                               615
278
279   GCC CCC CAA GTC CTC GAT ACG CAC TAT AGC ACC GAG AAT   1893
280   Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
281           620                               625                               630
282
283   GAC GTG GAG ACC ATC CGG GCC AGC GTC TGC GCC CCC TGC   1932
284   Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
285           635                               640
286
287   CAC GCC TCA TGT GCC ACA TGC CAG GGG CCG GCC CTG ACA   1971
288   His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
289   645                               650                               655
290
291   GAC TGC CTC AGC TGC CCC AGC CAC GCC TCC TTG GAC CCT   2010
292   Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
293           660                               665                               670
294
295   GTG GAG CAG ACT TGC TCC CGG CAA AGC CAG AGC AGC CGA   2049
296   Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg
297           675                               680
298
299   GAG TCC CCG CCA CAG CAG CAG CCA CCT CGG CTG CCC CCG   2088
300   Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro
301           685                               690                               695
302
303   GAG GTG GAG GCG GGG CAA CGG CTG CGG GCA GGG CTG CTG   2127
304   Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu
305           700                               705
306
307   CCC TCA CAC CTG CCT GAG GTG GTG GCC GGC CTC AGC TGC   2166
308   Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys
309   710                               715                               720
310
311   GCC TTC ATC GTG CTG GTC TTC GTC ACT GTC TTC CTG CTC   2205
312   Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val
313           725                               730                               735
314
315   CTG CAG CTG CGC TCT GGC TTT AGT TTT CGG GGG GTG AAG   2244
316   Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys
317           740                               745
318

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319 GTG TAC ACC ATG GAC CGT GGC CTC ATC TCC TAC AAG GGG 2283
320 Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly
321 750 755 760

323 CTG CCC CCT GAA GCC TGG CAG GAG GAG TGC CCG TCT GAC 2322
324 Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp
325 765 770

327 TCA GAA GAG GAC GAG GGC CGG GGC GAG AGG ACC GCC TTT 2361
328 Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
329 775 780 785

331 ATC AAA GAC CAG AGC GCC CTC TGA 2385
332 Ile Lys Asp Gln Ser Ala Leu End
333 790

(3) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 amino acids

(B) TYPE: amino acids

(C) STRANDEDNESS: single

(D) Topology: unknown

(ii) MOLECULE TYPE: furin

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) PUBLICATION INFORMATION: A.M.W. van den Ouweland et al,
Nucl. Acids. Res., 18:664 (1990)

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:2

360 Met Glu Leu Arg Pro Trp Leu
361 1 5

363 Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu
364 10 15 20

366 Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr
367 25 30

369 Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn
370 35 40 45

371

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372 Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln
373          50          55
374
375 Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val
376   60          65          70
377
378 Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser
379          75          80          85
380
381
382 Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln
383          90          95
384
385 Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln
386   100          105          110
387
388 Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu
389          115          120
390
391 Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala
392  125          130          135
393
394 Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser
395          140          145          150
396
397 Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu
398          155          160
399
400 Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn
401   165          170          175
402
403 Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met
404          180          185
405
406 Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val
407  190          195          200
408
409 Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val
410          205          210          215
411
412 Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp
413          220          225
414
415 Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly
416   230          235          240
417
418 Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp
419          245          250
420
421 Gly Pro Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala
422  255          260          265
423
424 Arg Leu Ala Glu Glu Ala Phe Phe Arg Gly Val Ser Gln

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425          270          275          280
426
427 Gly Arg Gly Gly Leu Gly Ser Ile Phe Val Trp Ala Ser
428          285          290
429
430 Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn Cys Asp
431          295          300          305
432
433 Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser
434          310          315
435
436
437 Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala
438          320          325          330
439
440 Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn
441          335          340          345
442
443 Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln
444          350          355
445
446 Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala
447          360          365          370
448
449 Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
450          375          380
451
452 Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val
453          385          390          395
454
455 Val Gln Thr Ser Lys Pro Ala His Leu Asn Ala Asn Asp
456          400          405          410
457
458 Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser
459          415          420
460
461 Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala
462          425          430          435
463
464 Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys
465          440          445
466
467 Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly
468          450          455          460
469
470 Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu
471          465          470          475
472
473 Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln
474          480          485
475
476 Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu
477          490          495          500

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478
479 Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr
480 505 510
481
482 Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly
483 515 520 525
484
485 Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp
486 530 535 540
487
488 Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn
489 545 550
490
491 Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe
492 555 560 565
493
494 Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro
495 570 575
496
497 Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
498 580 585 590
499
500 Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
501 595 600 605
502
503 His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
504 610 615
505
506 Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
507 620 625 630
508
509 Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
510 635 640
511
512 His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
513 645 650 655
514
515 Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
516 660 665 670
517
518 Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg
519 675 680
520
521 Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro
522 685 690 695
523
524 Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu
525 700 705
526
527 Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys
528 710 715 720
529
530 Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val

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531	725	730	735
532			
533	Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys		
534	740	745	
535			
536	Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly		
537	750	755	760
538			
539	Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp		
540	765	770	
541			
542	Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe		
543	775	780	785
544			
545			
546	Ile Lys Asp Gln Ser Ala Leu		
547	790		

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/621,092

DATE: 01/24/91
TIME: 08:58:37

LINE ERROR

ORIGINAL TEXT

36 Wrong application Serial Number
38 Wrong Filing Date
40 Wrong Classification
80 Extra Level-0 Records
355 Extra Level-0 Records

(A) APPLICATION NUMBER: 07/621092
(B) FILING DATE: 26-NOV-1990
(C) CLASSIFICATION: 424
al, Nucl. Acids. Res., 18:664 (1990)
Nucl. Acids. Res., 18:664 (1990)

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/621,092

DATE: 01/24/91
TIME: 08:58:37

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/621,092

DATE: 01/24/91
TIME: 08:58:37

LINE ORIGINAL TEXT

CORRECTED TEXT

48 (viii) ATTORNEY/AGENT INFORMATION
59 (2) INFORMATION FOR SEQ ID NO:1
82 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:1
336 (3) INFORMATION FOR SEQ ID NO:2
357 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:2

(viii) ATTORNEY/AGENT INFORMATION:
(2) INFORMATION FOR SEQ ID NO:1:
(vi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
(3) INFORMATION FOR SEQ ID NO:2:
(vi) SEQUENCE DESCRIPTION: SEQ ID NO:2: